



SEQUENCE LISTING

<10> Thomas, Susan Margaret  
<20> COMPOSITION AND METHOD FOR DETECTING MUTAGENS  
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Gly Ile Ser Asp Gly Asp Leu Leu Ile Val Asp Ser Ala Ile Thr Ala  
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Ser His Gly Asp Ile Val Ile Ala Ala Val Asp Gly Glu Phe Thr Val  
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Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro  
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Gln Lys Asn Gly Ile	Lys Val Asn Phe Lys	Ile Arg His Asn Ile Glu	
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Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly  
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Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro  
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Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser  
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 <212> PRT  
 <213> Enterobacteriaceae

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Gln Gly Tyr Glu Lys Gln Glu Leu Asn Leu His Glu Tyr Cys Val Arg  
 35 40 45

His Pro Ser Ala Thr Tyr Phe Leu Arg Val Ser Gly Ser Ser Met Glu  
 50 55 60

Asp Gly Arg Ile His Asp Gly Asp Val Leu Val Val Asp Arg Ser Leu  
 65 70 75 80

Thr Ala Ser His Gly Ser Ile Val Val Ala Cys Ile His Asn Glu Phe  
 85 90 95

Thr Val Lys Arg Leu Leu Leu Arg Pro Arg Pro Cys Leu Met Pro Met  
100 105 110

Asn Lys Asp Phe Pro Val Tyr Tyr Ile Asp Pro Asp Asn Glu Ser Val  
115 120 125

Glu Ile Trp Gly Val Val Thr His Ser Leu Ile Glu His Pro Val Cys  
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Leu Arg  
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<211> 421  
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<400> 12

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35 40 45

Leu Lys Met Gly Asp Pro Tyr Phe Lys Val Arg Pro Ile Ile Glu Arg  
50 55 60

His Asn Ile Ala Ile Phe Ser Ser Asn Tyr Thr Leu Tyr Ala Ser Met  
65 70 75 80

Ser Ala Arg Phe Ala Ala Val Val Glu Ser Leu Ala Ser His Val Glu  
85 90 95

Gln Tyr Ser Ile Asp Glu Leu Phe Val Asp Cys Lys Gly Ile Thr Ala  
100 105 110

Ala Met Ser Leu Asp Ala Phe Gly Arg Gln Leu Arg Glu Glu Val Arg  
115 120 125

Arg His Thr Thr Leu Val Cys Gly Val Gly Ile Ala Arg Thr Lys Thr  
130 135 140

Leu Ala Lys Leu Cys Asn His Ala Ala Lys Thr Trp Pro Ala Thr Gly

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Gly Val Val Ala Leu Asp Asp Gly Ala Arg Leu Lys Lys Leu Met Ser						
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Ile Leu Pro Val Ala Glu Val Trp Gly Val Gly His Arg Thr Glu Lys						
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Ala Leu Ala Thr Met Gly Ile Lys Thr Val Leu Asp Leu Ala Arg Ala						
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Asp Thr Arg Leu Ile Arg Lys Thr Phe Gly Val Val Leu Glu Arg Thr						
	210			215		220
Val Arg Glu Leu Arg Gly Glu Ala Cys Phe Ser Leu Glu Glu Asn Pro						
	225			230		235
Pro Ala Lys Gln Gln Ile Val Val Ser Arg Ser Phe Gly Gln Arg Val						
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Glu Thr Leu Thr Asp Met Gln Gln Ala Val Thr Gly Phe Ala Ala Arg						
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Ala Ala Glu Lys Leu Arg Asn Glu Arg Gln Tyr Cys Arg Val Ile Ser						
	275			280		285
Val Phe Ile Arg Thr Ser Pro Tyr Ser Val Arg Asp Thr Gln Tyr Ala						
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Asn Gln Ala Thr Glu Lys Leu Thr Val Ala Thr Gln Asp Ser Arg Thr						
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Ile Ile Gln Ala Ala Gln Ala Ala Leu Ala Arg Ile Trp Arg Glu Asp						
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Ile Ala Tyr Ala Lys Ala Gly Val Met Leu Ala Asp Phe Ser Gly Lys						
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Glu Ala Gln Leu Asp Leu Phe Asp Ser Ala Thr Pro Ser Ala Gly Ser						
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Glu Ala Leu Met Ala Val Leu Asp Gly Ile Asn Arg Arg Gly Lys Asn						
	370			375		380
Gln Leu Phe Phe Ala Gly Gln Gly Ile Asp Asn Ser Phe Ala Met Arg						

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Arg Gln Met Leu Ser Pro Asp Tyr Thr Thr Asp Trp Arg Ser Ile Pro  
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Ile Ala Thr Ile Lys  
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<211> 74  
<212> PRT  
<213> Enterobacteriaceae

<400> 13

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Glu Lys Leu Phe Ser Asn Glu Leu Pro Pro Cys Leu Ile Thr Leu Gln  
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Arg Glu Lys Arg Thr Tyr Gly Tyr Cys Ser Phe Lys Arg Phe Val Gly  
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Arg Glu Ser Gly Tyr Thr Val Asp Glu Ile  
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35 40 45

His Pro Ser Ala Thr Tyr Phe Leu Arg Val Ser Gly Ser Ser Met Glu  
50 55 60

Asp Gly Arg Ile His Asp Gly Asp Val Leu Val Val Asp Arg Ser Leu  
65 70 75 80

Thr Ala Ser His Gly Ser Ile Val Val Ala Cys Ile His Asn Glu Phe  
85 90 95

Thr Val Lys Arg Leu Leu Leu Arg Pro Arg Pro Cys Leu Met Pro Met  
100 105 110

Asn Lys Asp Phe Pro Val Tyr Tyr Ile Asp Pro Asp Asn Glu Ser Val  
115 120 125

Glu Ile Trp Gly Val Val Thr His Ser Leu Ile Glu His Pro Val Cys  
130 135 140

Leu Arg  
145

<210> 16  
<211> 420  
<212> PRT  
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20 25 30

Asn Asp Gly Asn Ile Val Ala Arg Asn Tyr Leu Ala Lys Lys Ala Gly  
35 40 45

Leu Lys Met Gly Asp Pro Tyr Phe Lys Val Arg Pro Ile Ile Glu Arg  
18

50

55

60

His Asn Ile Ala Ile Phe Ser Ser Asn Tyr Thr Leu Tyr Ala Ser Met  
65 70 75 80

Ser Ala Arg Phe Ala Ala Val Val Glu Ser Leu Ala Ser His Val Glu  
85 90 95

Gln Tyr Ser Ile Asp Glu Leu Phe Val Asp Cys Lys Gly Ile Thr Ala  
100 105 110

Ala Met Ser Leu Asp Ala Phe Gly Arg Gln Leu Arg Glu Glu Val Arg  
115 120 125

Arg His Thr Thr Leu Val Cys Gly Val Gly Ile Ala Arg Thr Lys Thr  
130 135 140

Leu Ala Lys Leu Cys Asn His Ala Ala Lys Thr Trp Pro Ala Thr Gly  
145 150 155 160

Gly Val Val Ala Leu Asp Asp Gly Ala Arg Leu Lys Lys Leu Met Ser  
165 170 175

Ile Leu Pro Val Ala Glu Val Trp Gly Val Gly His Arg Thr Glu Lys  
180 185 190

Ala Leu Ala Thr Met Gly Ile Lys Thr Val Leu Asp Leu Ala Arg Ala  
195 200 205

Asp Thr Arg Leu Ile Arg Lys Thr Phe Gly Val Val Leu Glu Arg Thr  
210 215 220

Val Arg Glu Leu Arg Gly Glu Ala Cys Phe Ser Leu Glu Glu Asn Pro  
225 230 235 240

Pro Ala Lys Gln Gln Ile Val Val Ser Arg Ser Phe Gly Gln Arg Val  
245 250 255

Glu Thr Leu Thr Asp Met Gln Gln Ala Val Thr Gly Phe Ala Ala Arg  
260 265 270

Ala Ala Glu Lys Leu Arg Asn Glu Arg Gln Tyr Cys Arg Val Ile Ser  
275 280 285

Val Phe Ile Arg Thr Ser Pro Tyr Ser Val Arg Asp Thr Gln Tyr Ala

290

295

300

Asn Gln Ala Thr Glu Lys Leu Thr Val Ala Thr Gln Asp Ser Arg Thr  
305 310 315 320

Ile Ile Gln Ala Ala Gln Ala Leu Ala Arg Ile Trp Arg Glu Asp Ile  
325 330 335

Ala Tyr Ala Lys Ala Gly Val Met Leu Ala Asp Phe Ser Gly Lys Glu  
340 345 350

Ala Gln Leu Asp Leu Phe Asp Ser Ala Thr Pro Ser Ala Gly Ser Glu  
355 360 365

Ala Leu Met Ala Val Leu Asp Gly Ile Asn Arg Arg Gly Lys Asn Gln  
370 375 380

Leu Phe Phe Ala Gly Gln Gly Ile Asp Asn Ser Phe Ala Met Arg Arg  
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Gln Met Leu Ser Pro Asp Tyr Thr Thr Asp Trp Arg Ser Ile Pro Ile  
405 410 415

Ala Thr Ile Lys  
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aagatttaaa cagtcgtagc gactccggta tcttgcgcg atgttcaa aacactactg 180  
tatataaaaa cagtattcga ggtatggatt atg gaa ttt ttc aga cct aca gag 234

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Leu Arg Glu Ile Ile Pro Leu Pro Phe Phe Ser Tyr Leu Val Pro Cys									
10 15 20									
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Gly Phe Pro Ser Pro Ala Ala Asp Tyr Ile Glu Gln Arg Ile Asp Leu									
25 30 35 40									
aat gag ttg ctc gtt tct cat ccc agc tca aca tat ttt gtc aaa gcc									378
Asn Glu Leu Leu Val Ser His Pro Ser Ser Thr Tyr Phe Val Lys Ala									
45 50 55									
tcg ggg gat tca atg att gaa gca ggc atc agc gac ggt gac ctg ctg									426
Ser Gly Asp Ser Met Ile Glu Ala Gly Ile Ser Asp Gly Asp Leu Leu									
60 65 70									
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Val Val Asp Ser Ser Arg Asn Ala Asp His Gly Asp Ile Val Ile Ala									
75 80 85									
gca att gaa gga gag ttc acc gta aaa cgg ttg cag ttg cgc ccg aca									522
Ala Ile Glu Gly Glu Phe Thr Val Lys Arg Leu Gln Leu Arg Pro Thr									
90 95 100									
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Val Gln Leu Ile Pro Met Asn Gly Ala Tyr Arg Pro Ile Pro Val Gly									
105 110 115 120									
agt gaa gac acg ctc gac ata ttc ggg gtg gtg acc ttt atc att aaa									618
Ser Glu Asp Thr Leu Asp Ile Phe Gly Val Val Thr Phe Ile Ile Lys									
125 130 135									
gcg gtc agt tga tt atg ttc gcg ctc tgc gat gtt aat agc ttt tac									665
Ala Val Ser Met Phe Ala Leu Cys Asp Val Asn Ser Phe Tyr									
140 145 150									
gcc tcc tgc gaa acg gtc ttt cgt cct gat tta tgt ggc cga ccg gtg									713
Ala Ser Cys Glu Thr Val Phe Arg Pro Asp Leu Cys Gly Arg Pro Val									
155 160 165									
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Val Val Leu Ser Asn Asn Asp Gly Cys Val Ile Ala Cys Ser Ala Glu									
170 175 180									
gcg aaa cag ctc ggt atc gca cca ggt gag cca tac ttc aaa cag aaa									809
Ala Lys Gln Leu Gly Ile Ala Pro Gly Glu Pro Tyr Phe Lys Gln Lys									
185 190 195									
gaa cgc ttc cgg cga tcc ggt gtt gtt tgc ttc agc agt aat tac gag									857
Glu Arg Phe Arg Arg Ser Gly Val Val Cys Phe Ser Ser Asn Tyr Glu									
200 205 210									
ctt tac gct gat atg tcg aac cgg gta atg acc aca ctc gag gag atg									905
Leu Tyr Ala Asp Met Ser Asn Arg Val Met Thr Thr Leu Glu Glu Met									
215 220 225 230									
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Thr	Gly	Val	Arg	Asn	Cys	Arg	Asp	Leu	Thr	Asp	Phe	Gly	Arg	Glu	Ile	
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aga	gcg	acg	gtc	ctg	aag	cgc	acg	cac	ctg	act	gtc	ggg	gta	ggc	att	1049
Arg	Ala	Thr	Val	Leu	Lys	Arg	Thr	His	Leu	Thr	Val	Gly	Val	Gly	Ile	
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gcc	cag	acg	aaa	acc	ctt	gcc	aag	ctg	gct	aac	cat	gct	gcg	aaa	aag	1097
Ala	Gln	Thr	Lys	Thr	Leu	Ala	Lys	Leu	Ala	Asn	His	Ala	Ala	Lys	Lys	
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tgg	cag	cgc	cag	acc	gac	ggg	gtg	ggt	gac	ttg	tcg	aac	atc	gat	cgc	1145
Trp	Gln	Arg	Gln	Thr	Asp	Gly	Val	Val	Asp	Leu	Ser	Asn	Ile	Asp	Arg	
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cag	cgt	cgg	ctg	ctg	gcc	ctg	ata	ccc	gtg	gag	gat	gtc	tgg	ggg	gtc	1193
Gln	Arg	Arg	Leu	Leu	Ala	Leu	Ile	Pro	Val	Glu	Asp	Val	Trp	Gly	Val	
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ggc	agg	cgc	atc	agt	aag	aag	ctc	aat	gcc	ctg	ggc	atc	aag	act	gct	1241
Gly	Arg	Arg	Ile	Ser	Lys	Lys	Leu	Asn	Ala	Leu	Gly	Ile	Lys	Thr	Ala	
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ctc	gat	ctc	tct	gaa	caa	agt	acc	tgg	atc	atc	agg	aaa	cac	ttc	aat	1289
Leu	Asp	Leu	Ser	Glu	Gln	Ser	Thr	Trp	Ile	Ile	Arg	Lys	His	Phe	Asn	
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gtc	gtg	ctg	gag	cgt	acc	gtg	aga	gag	ctt	cgc	gga	gag	cca	tgt	ctg	1337
Val	Val	Leu	Glu	Arg	Thr	Val	Arg	Glu	Leu	Arg	Gly	Glu	Pro	Cys	Leu	
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gag	ctc	gaa	gag	ttt	gcg	ccg	gca	aag	cag	gaa	atc	gtt	tgt	agt	cgc	1385
Glu	Leu	Glu	Glu	Phe	Ala	Pro	Ala	Lys	Gln	Glu	Ile	Val	Cys	Ser	Arg	
375					380					385					390	
tct	ttc	ggc	gag	cgg	gtc	aca	gac	tat	gag	gaa	atg	cgc	cag	gct	gtt	1433
Ser	Phe	Gly	Glu	Arg	Val	Thr	Asp	Tyr	Glu	Glu	Met	Arg	Gln	Ala	Val	
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Tyr	Ser	Tyr	Ala	Ala	Arg	Ala	Ala	Glu	Lys	Leu	Arg	Gly	Glu	His	Gln	
			410					415					420			
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Tyr	Cys	Arg	Phe	Ile	Ser	Thr	Phe	Val	Lys	Thr	Ser	Pro	Phe	Ala	Leu	
		425					430					435				
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Asn	Glu	Pro	Tyr	Tyr	Gly	Asn	Ser	Ala	Ala	Val	Thr	Leu	Leu	Thr	Pro	
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Thr	Gln	Asp	Ser	Arg	Asp	Ile	Ile	Asn	Ala	Ala	Val	Lys	Cys	Leu	Asp	
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Gly Asp Phe Phe Ser Gln Gly Val Ala Gln Leu Asn Leu Phe Asp Asp	
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Asn Ala Pro Arg Ala Gly Ser Ala Lys Leu Met Glu Val Leu Asp His	
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Leu Asn Ala Lys Asp Gly Lys Gly Thr Leu Tyr Phe Ala Gly Gln Gly	
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Met Ser Gln Gln Trp Ala Met Lys Arg Glu Met Leu Ser Pro Arg Tyr	
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Thr Thr Arg Tyr Ser Asp Leu Leu Arg Val Lys	
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acgacgaaaa tcaactggttt agtaaaatgg tttaaccctg aaaagggtt tggtttcatt	2511
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ttc	2574

<210> 18  
 <211> 139  
 <212> PRT  
 <213> Salmonella typhimurium

<400> 18

Met Glu Phe Phe Arg Pro Thr Glu Leu Arg Glu Ile Ile Pro Leu Pro
1 5 10 15

Phe Phe Ser Tyr Leu Val Pro Cys Gly Phe Pro Ser Pro Ala Ala Asp

20                                      25                                      30  
 Tyr Ile Glu Gln Arg Ile Asp Leu Asn Glu Leu Leu Val Ser His Pro  
           35                                      40                                      45  
 Ser Ser Thr Tyr Phe Val Lys Ala Ser Gly Asp Ser Met Ile Glu Ala  
           50                                      55                                      60  
 Gly Ile Ser Asp Gly Asp Leu Leu Val Val Asp Ser Ser Arg Asn Ala  
           65                                      70                                      75                                      80  
 Asp His Gly Asp Ile Val Ile Ala Ala Ile Glu Gly Glu Phe Thr Val  
                                   85                                      90                                      95  
 Lys Arg Leu Gln Leu Arg Pro Thr Val Gln Leu Ile Pro Met Asn Gly  
                                   100                                      105                                      110  
 Ala Tyr Arg Pro Ile Pro Val Gly Ser Glu Asp Thr Leu Asp Ile Phe  
                                   115                                      120                                      125  
 Gly Val Val Thr Phe Ile Ile Lys Ala Val Ser  
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<210> 19  
 <211> 422  
 <212> PRT  
 <213> Salmonella typhimurium

<400> 19

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 Val Phe Arg Pro Asp Leu Cys Gly Arg Pro Val Val Val Leu Ser Asn  
                                   20                                      25                                      30  
 Asn Asp Gly Cys Val Ile Ala Cys Ser Ala Glu Ala Lys Gln Leu Gly  
                                   35                                      40                                      45  
 Ile Ala Pro Gly Glu Pro Tyr Phe Lys Gln Lys Glu Arg Phe Arg Arg  
                                   50                                      55                                      60  
 Ser Gly Val Val Cys Phe Ser Ser Asn Tyr Glu Leu Tyr Ala Asp Met  
 65                                      70                                      75                                      80  
 Ser Asn Arg Val Met Thr Thr Leu Glu Glu Met Val Pro Arg Val Glu  
                                   85                                      90                                      95



Ile Tyr Ser Ile Asp Glu Ala Phe Cys Asp Leu Thr Gly Val Arg Asn  
 100 105 110  
 Cys Arg Asp Leu Thr Asp Phe Gly Arg Glu Ile Arg Ala Thr Val Leu  
 115 120 125  
 Lys Arg Thr His Leu Thr Val Gly Val Gly Ile Ala Gln Thr Lys Thr  
 130 135 140  
 Leu Ala Lys Leu Ala Asn His Ala Ala Lys Lys Trp Gln Arg Gln Thr  
 145 150 155 160  
 Asp Gly Val Val Asp Leu Ser Asn Ile Asp Arg Gln Arg Arg Leu Leu  
 165 170 175  
 Ala Leu Ile Pro Val Glu Asp Val Trp Gly Val Gly Arg Arg Ile Ser  
 180 185 190  
 Lys Lys Leu Asn Ala Leu Gly Ile Lys Thr Ala Leu Asp Leu Ser Glu  
 195 200 205  
 Gln Ser Thr Trp Ile Ile Arg Lys His Phe Asn Val Val Leu Glu Arg  
 210 215 220  
 Thr Val Arg Glu Leu Arg Gly Glu Pro Cys Leu Glu Leu Glu Glu Phe  
 225 230 235 240  
 Ala Pro Ala Lys Gln Glu Ile Val Cys Ser Arg Ser Phe Gly Glu Arg  
 245 250 255  
 Val Thr Asp Tyr Glu Glu Met Arg Gln Ala Val Tyr Ser Tyr Ala Ala  
 260 265 270  
 Arg Ala Ala Glu Lys Leu Arg Gly Glu His Gln Tyr Cys Arg Phe Ile  
 275 280 285  
 Ser Thr Phe Val Lys Thr Ser Pro Phe Ala Leu Asn Glu Pro Tyr Tyr  
 290 295 300  
 Gly Asn Ser Ala Ala Val Thr Leu Leu Thr Pro Thr Gln Asp Ser Arg  
 305 310 315 320  
 Asp Ile Ile Asn Ala Ala Val Lys Cys Leu Asp Lys Ile Trp Arg Asp  
 325 330 335

Gly His Arg Tyr Gln Lys Ala Gly Val Met Leu Gly Asp Phe Phe Ser  
 340 345 350

Gln Gly Val Ala Gln Leu Asn Leu Phe Asp Asp Asn Ala Pro Arg Ala  
 355 360 365

Gly Ser Ala Lys Leu Met Glu Val Leu Asp His Leu Asn Ala Lys Asp  
 370 375 380

Gly Lys Gly Thr Leu Tyr Phe Ala Gly Gln Gly Met Ser Gln Gln Trp  
 385 390 395 400

Ala Met Lys Arg Glu Met Leu Ser Pro Arg Tyr Thr Thr Arg Tyr Ser  
 405 410 415

Asp Leu Leu Arg Val Lys  
 420

<210> 20  
 <211> 2138  
 <212> DNA  
 <213> Salmonella typhimurium

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 tgccgttatc atatatactg tataaatgta cagctaagga gaggcattaa tgtcactaaa 180  
 acctatgaaa tcagcccctg acaccaaaga aactatccct ttctttggcg agctcgtacc 240  
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 ggtggttact catccagcca gcacgtactt cttgcgcgtg acaggtgact ccatgcagga 360  
 tgctcggata cattctgggtg acgtgctggt ggttgatcgc tcagaaactc cagagcaggg 420  
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 acgtccatgc cttatgccga tgaacccggc ataccacact atctattttg accctgaaag 540  
 taacgacgtt gaaatttggg gtgtggtgac ttactcatta atgaagcaca aaaaatgtat 600  
 ggctgatcg acattaattc ctgctactgt gcctgcgagc aagcattcag gcccgatctt 660  
 gctggtaaac ccgtagtagt tttgtcaaac aatgatgcca gctgcatagc ccgtaacaag 720  
 caggcgaaag cccttggtat aaaaatgggc gagccattct ttaaaatcaa agatctcata 780  
 gaacggaaca atgtcgtgtg tttcagttca aactatgccc tttattccgc atttagttcc 840

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cagcaagcca taaccgatta tgcggctcgc gctgccgaaa aactccggca agaaaaaggg 1440
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tattccaatc aggctactga aatgctggtg actccctcca acgacagcag ggatattatt 1560
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tgtgatgctt tgtgatattc gcgagcgtga gcctcaactt gatttgttca ctgaatcggc 1680
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gctatcccct gcatatttga ctaggctggg atgatttacc aaagggttagg ttaggataag 1860
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gtccggcagc gcaatttggg tctcaagggt acgtgttcaa aaacagctat aagattatgg 1980
tcacgcgctg taagccatgc cagaactaaa taaattggat tttttcgtaa tgaaaatata 2040
gcgacgaacg ttgcaaaaact gttttattgc tacaattccc cttgttggct aaaatacata 2100
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<210> 21
<211> 145
<212> PRT
<213> Salmonella typhimurium

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<400> 21

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Met Ser Leu Lys Pro Met Lys Ser Ala Pro Asp Thr Lys Glu Thr Ile
1           5           10           15

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Pro Phe Phe Gly Glu Leu Val Pro Ala Gly Phe Pro Ser Pro Ala Ala
20           25           30

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Gly Trp Glu Glu Ala Glu Leu Asn Leu His Thr Leu Val Val Thr His  
35 40 45

Pro Ala Ser Thr Tyr Phe Leu Arg Val Thr Gly Asp Ser Met Gln Asp  
50 55 60

Ala Arg Ile His Ser Gly Asp Val Leu Val Val Asp Arg Ser Glu Thr  
65 70 75 80

Pro Glu Gln Gly Ser Ile Val Val Ala Ser Ile Asp Asn Glu Phe Thr  
85 90 95

Val Lys Lys Leu Ile Leu Arg Pro Arg Pro Cys Leu Met Pro Met Asn  
100 105 110

Pro Ala Tyr Pro Pro Ile Tyr Phe Asp Pro Glu Ser Asn Asp Val Glu  
115 120 125

Ile Trp Gly Val Val Thr Tyr Ser Leu Met Lys His Lys Lys Cys Met  
130 135 140

Ala  
145

<210> 22  
<211> 339  
<212> PRT  
<213> Salmonella typhimurium

<400> 22

Met Tyr Gly Leu Ile Asp Ile Asn Ser Cys Tyr Cys Ala Cys Glu Gln  
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Ala Phe Arg Pro Asp Leu Ala Gly Lys Pro Val Val Val Leu Ser Asn  
20 25 30

Asn Asp Ala Ser Cys Ile Ala Arg Asn Lys Gln Ala Lys Ala Leu Gly  
35 40 45

Ile Lys Met Gly Glu Pro Phe Phe Lys Ile Lys Asp Leu Ile Glu Arg  
50 55 60

Asn Asn Val Ala Val Phe Ser Ser Asn Tyr Ala Leu Tyr Ser Ala Phe  
65 70 75 80

Ser Ser Arg Phe Ala Ser Val Ile Glu Ser Leu Thr Pro Arg Ser Ser

85

90

95

Val Tyr Ser Ile Asp Glu Leu Trp Phe Asp Ala Thr Asn Ile Thr Gly  
 100 105 110

Leu Met Thr Leu Asp Ala Tyr Gly Arg Met Leu Arg Glu Glu Val Gln  
 115 120 125

Arg Gln Thr Thr Leu Thr Cys Gly Val Gly Ile Ala Pro Thr Lys Thr  
 130 135 140

Leu Ala Lys Leu Cys Ser His Ala Ser Lys Thr Tyr Pro Ala Thr Gly  
 145 150 155 160

Gly Val Val Ala Leu Asp Asp Val Thr Arg Leu Glu Lys Leu Met Arg  
 165 170 175

Leu Val Pro Val Glu Asp Val Trp Gly Val Gly Pro Arg Leu Gly Lys  
 180 185 190

Arg Leu Arg Phe Met Gly Val Glu Thr Ala Phe Gln Leu Ser Cys Leu  
 195 200 205

Asp Pro Val Arg Val Arg Lys Gln Phe Asn Val Val Leu Glu Arg Thr  
 210 215 220

Val Arg Glu Leu Arg Gly Glu Pro Cys Met Ala Leu Asp Glu Asn Asp  
 225 230 235 240

Val Met Lys Gln Gln Ile Val Val Ser Arg Ser Phe Gly Glu Arg Val  
 245 250 255

Thr Asn Leu His Glu Met Gln Gln Ala Ile Thr Asp Tyr Ala Ala Arg  
 260 265 270

Ala Ala Glu Lys Leu Arg Gln Glu Lys Gly Tyr Val Ser Val Ile Gly  
 275 280 285

Val Phe Ile Arg Thr Ser Pro Tyr Ala Val Asn Asp Val Pro Tyr Ser  
 290 295 300

Asn Gln Ala Thr Glu Met Leu Val Thr Pro Ser Asn Asp Ser Arg Asp  
 305 310 315 320

Ile Ile Asn Ala Ala Gln Arg Ala Leu Thr Asp Leu Glu Ala Arg Ser

325

330

335

Pro Leu Cys

<210> 23  
 <211> 736  
 <212> DNA  
 <213> *Aequorea victoria*

<220>  
 <221> CDS  
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<400> 23  
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                   1                  5                  10

cca att ttg gtt gaa tta gat ggt gat gtt aat ggt cac aaa ttt tct 97  
 Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser  
                   15                  20                  25

gtc tcc ggt gaa ggt gaa ggt gat gct act tac ggt aaa ttg acc tta 145  
 Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu  
                   30                  35                  40

aaa ttt att tgt act act ggt aaa ttg cca gtt cca tgg cca acc tta 193  
 Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu  
                   45                  50                  55                  60

gtc act act ttc ggt tat ggt gtt caa tgt ttt gct aga tac cca gat 241  
 Val Thr Thr Phe Gly Tyr Gly Val Gln Cys Phe Ala Arg Tyr Pro Asp  
                   65                  70                  75

cat atg aaa caa cat gac ttt ttc aag tct gcc atg cca gaa ggt tat 289  
 His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr  
                   80                  85                  90

gtt caa gaa aga act att ttt ttc aaa gat gac ggt aac tac aag acc 337  
 Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr  
                   95                  100                  105

aga gct gaa gtc aag ttt gaa ggt gat acc tta gtt aat aga atc gaa 385  
 Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu  
                   110                  115                  120

tta aaa ggt att gat ttt aaa gaa gat ggt aac att tta ggt cac aaa 433  
 Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys  
                   125                  130                  135                  140

ttg gaa tac aac tat aac tct cac aat gtt tac atc atg gct gac aaa 481  
 Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys  
                   145                  150                  155

caa aag aat ggt atc aaa gtt aac ttc aaa att aga cac aac att gaa 529

Gln	Lys	Asn	Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu		
			160					165					170				
gat	ggt	tct	gtt	caa	tta	gct	gac	cat	tat	caa	caa	aat	act	cca	att	577	
Asp	Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile		
		175					180					185					
ggt	gat	ggt	cca	gtc	ttg	tta	cca	gac	aac	cat	tac	tta	tcc	act	caa	625	
Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln		
	190					195					200						
tct	gcc	tta	tcc	aaa	gat	cca	aac	gaa	aag	aga	gac	cac	atg	gtc	ttg	673	
Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu		
205					210					215					220		
tta	gaa	ttt	gtt	act	gct	gct	ggt	att	acc	cat	ggt	atg	gat	gaa	ttg	721	
Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	Leu		
				225					230					235			
tac	aaa	taa	ctgcag													736	
Tyr	Lys																

<210> 24  
 <211> 238  
 <212> PRT  
 <213> Aequorea victoria

<400> 24

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Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu		
		20						25					30				
Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys		
		35					40					45					
Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Phe		
	50					55					60						
Gly	Tyr	Gly	Val	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln		
65					70				75						80		
His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg		
				85					90					95			
Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val		
			100					105						110			
Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile		

115	120	125
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn		
130	135	140
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly		
145	150	155
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val		
165	170	175
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro		
180	185	190
Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser		
195	200	205
Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val		
210	215	220
Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys		
225	230	235